Recitation of the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

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Claims 1-35 (cancelled)

MB

36. (**Currently Amended**) A method for generating of at least one non-naturally occurring variant protein with at least one desired characteristic relative to a target protein comprising:

a) inputting the coordinates of said target protein into a computer;

b) identifying a plurality of variable residue positions in said target protein based upon said at least one desired characteristic;

c) applying a force field calculation to said plurality of variable residue positions and said coordinates to generate a primary library comprising optimized variant protein sequences;

d) generating a set of amino acid residues at each of said plurality of variable residue positions by combining:

(i) at least one variant amino acid in said primary library at said variable residue position, and

(ii) the amino acid residue of said target protein at said variable residue position;

e) generating a plurality of protein sequences by combining into the sequence of said target protein each of said set of amino acid residues at each of said plurality of variable residue positions to generate a secondary library of protein sequences, wherein at least one member of said secondary library is not found in said primary library, and wherein at least one member of said secondary library comprises a plurality of ~~variable~~ **variant** amino acids relative to said target protein; and

f) synthesizing a plurality of said secondary library protein sequences and screening said sequences to identify at least one non-naturally occurring variant protein with said at least one desired characteristic.

37. (Previously Presented) A method according to claim 36, wherein said force field calculation is a Self-Consistent Mean Field (SCMF) calculation.

38. (Previously Presented) A method according to claim 36 wherein said recombining comprises:

a) generating a set of oligonucleotide probes each encoding at least one of said amino acid residues at said variant positions;

b) using said probes in a polymerase chain reaction (PCR) to generate a plurality of oligonucleotide sequences, each encoding said secondary variant sequences; and

c) producing said secondary variant sequences in host cells transformed with said oligonucleotide sequences.

39. (Previously Presented) A method according to claim 38 wherein said PCR is multiple PCR wherein said probes are pooled.

40. (Previously Presented) A method according to 39 wherein said probes are added in equimolar amounts.

41. (Previously Presented) A method according to claim 39 wherein said probes are combined in amounts that correspond to the frequency of the said amino acid residues at said variant positions in said secondary library.